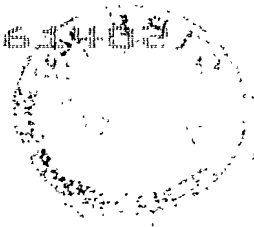


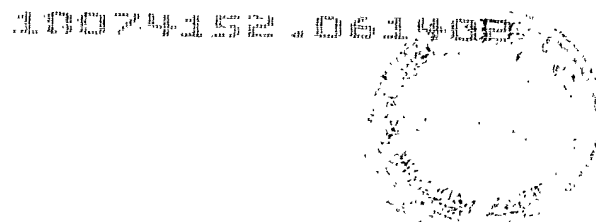
|                    |                     |                                |
|--------------------|---------------------|--------------------------------|
| 1 MMQKLQMYVY 10    | 11 IYLFMLIAAG 20    | 21 PV——DLNEGSE 30 Mouse        |
| 1 M I QKPQMYVY 10  | 11 IYLFVLI AAG 20   | 21 PV——DLNEDSE 30 Rat          |
| 1 -M QKLQ L CVY 9  | 10 IYLFMLI VAG 19   | 20 PV——DLNENSEQ 29 Human       |
| 1 -M QKLQ L CVY 9  | 10 IYLFMLI VAG 19   | 20 PV——DLNENSEQ 29 Baboon      |
| 1 -M QKLQ I SVY 9  | 10 IYLFMLI VAG 19   | 20 PV——DLNENSEQ 29 Bovine      |
| 1 -M QKLQ I YVY 9  | 10 IYLFMLI VAG 19   | 20 PV——DLNENSEQ 29 Porcine     |
| 1 -M QKLQ I FVY 9  | 10 IYLFMLL VAG 19   | 20 PV——DLNENSEQ 29 Ovine       |
| 1 -M QKLA VYVY 9   | 10 IYLFMQI AVD 19   | 20 PV——ALDGSSQP 29 Chicken     |
| 1 -M Q I LA VYVY 9 | 10 IYLFMQ I LVH 19  | 20 PV——ALDGSSQP 29 Turkey      |
| 1 -MH FTQ——VL 7    | 8 ISLS VL I ACG 17  | 18 PVGYGDITAHQQP 30 Zebrafish  |
| 31 EENVEKEGLC 40   | 41 NACA WRQNTR 50   | 51 YS RI E AIKIQ 60 Mouse      |
| 31 EANVEKEGLC 40   | 41 NACA WRQNTR 50   | 51 YS RI E AIKIQ 60 Rat        |
| 30 KENVEKEGLC 39   | 40 NACT WRQNTK 49   | 50 SS RI E AIKIQ 59 Human      |
| 30 KENVEKEGLC 39   | 40 NACT WRQNTK 49   | 50 SS RI E AIKIQ 59 Baboon     |
| 30 KENVEKEGLC 39   | 40 NACL WRE NTT 49  | 50 SS RLE AIKIQ 59 Bovine      |
| 30 KENVEKEGLC 39   | 40 NACMWRQNTK 49    | 50 SS RLE AIKIQ 59 Porcine     |
| 30 KENVEKKGLC 39   | 40 NACL WRQNNK 49   | 50 SS RLE AIKIQ 59 Ovine       |
| 30 TENAEKDGLC 39   | 40 NACT WRQNTK 49   | 50 SS RI E AIKIQ 59 Chicken    |
| 30 TENAEKDGLC 39   | 40 NACT WRQNTK 49   | 50 SS RI E AIKIQ 59 Turkey     |
| 31 STAT EES ELC 40 | 41 S TCE FRQHSK 50  | 51 LM RLHAISQ 60 Zebrafish     |
| 61 ILSKLRLETA 70   | 71 PNISKDA IRQ 80   | 81 LLPRAPPLRE 90 Mouse         |
| 61 ILSKLRLETA 70   | 71 PNISKDA IRQ 80   | 81 LLPRAPPLRE 90 Rat           |
| 60 ILSKLRLETA 69   | 70 PNISKDV IRQ 79   | 80 LLPKAPPLRE 89 Human         |
| 60 ILSKLRLETA 69   | 70 PNISKDA IRQ 79   | 80 LLPKAPPLRE 89 Baboon        |
| 60 ILSKLRLETA 69   | 70 PNISKDA IRQ 79   | 80 LLPRAPPLLE 89 Bovine        |
| 60 ILSKLRLETA 69   | 70 PNISKDA IRQ 79   | 80 LLPRAPPLRE 89 Porcine       |
| 60 ILSKLRLETA 69   | 70 PNISKDA IRQ 79   | 80 LLPRAPPLRE 89 Ovine         |
| 60 ILSKLRLEQA 69   | 70 PNISRDV IKQ 79   | 80 LLPRAPPLQE 89 Chicken       |
| 60 ILSKLRLEQA 69   | 70 PNISRDV IKQ 79   | 80 LLPRAPPLQE 89 Turkey        |
| 61 ILSKLRLEQA 70   | 71 PNISRDVVQK 80    | 81 LLPRAPPLQ 90 Zebrafish      |
| 91 LI DQYDVQRD 100 | 101 DS SDGSLEDD 110 | 111 DYH ATTET I I 120 Mouse    |
| 91 LI DQYDVQRD 100 | 101 DS SDGSLEDD 110 | 111 DYH ATTET I I 120 Rat      |
| 90 LI DQYDVQRD 99  | 100 DS SDGSLEDD 109 | 110 DYH ATTET I I 119 Human    |
| 90 LI DQYDVQRD 99  | 100 DS SDGSLEDD 109 | 110 DYH ATTET I I 119 Baboon   |
| 90 LI DQYDVQRD 99  | 100 AS SDGSLEDD 109 | 110 DYH ARTETV I 119 Bovine    |
| 90 LI DQYDVQRD 99  | 100 DS SDGSLEDD 109 | 110 DYH ATTET I I 119 Porcine  |
| 90 LI DQYDVQRD 99  | 100 DS SDGSLEDD 109 | 110 DYH VTTETV I 119 Ovine     |
| 90 LI DQYDVQRD 99  | 100 DS SDGSLEDD 109 | 110 DYH ATTET I I 119 Chicken  |
| 90 LI DQYDVQRD 99  | 100 DS SDGSLEDD 109 | 110 DYH ATTET I I 119 Turkey   |
| 91 LLDQYDVLGD 100  | 101 DSKDGAVEED 110  | 111 DEH ATTET IM 120 Zebrafish |

FIG. 1A



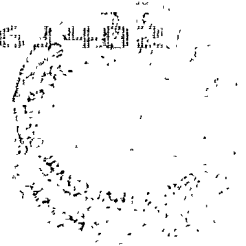
|                      |                      |                               |
|----------------------|----------------------|-------------------------------|
| 121 TMPTESDFLM 130   | 131 QADGKPKCCF 140   | 141 FKFSSKIQYN 150 Mouse      |
| 121 TMPTESDFLM 130   | 131 QADGKPKCCF 140   | 141 FKFSSKIQYN 150 Rat        |
| 120 TMPTESDFLM 129   | 130 QVDGKPKCCF 139   | 140 FKFSSKIQYN 149 Human      |
| 120 TMPTESDFLM 129   | 130 QVDGKPKCCF 139   | 140 FKFSSKIQYN 149 Baboon     |
| 120 TMPTESDLL T 129  | 130 QVEGKPKCCF 139   | 140 FKFSSKIQYN 149 Bovine     |
| 120 TMPTESDLLM 129   | 130 QVEGKPKCCF 139   | 140 FKFSSKIQYN 149 Porcine    |
| 120 TMPTESDLL A 129  | 130 EVQEKPKCCF 139   | 140 FKFSSKIQHN 149 Ovine      |
| 120 TMPTESDFL V 129  | 130 QMEGKPKCCF 139   | 140 FKFSSKIQYN 149 Chicken    |
| 120 TMPTESDFL V 129  | 130 QMEGKPKCCF 139   | 140 FKFSSKIQYN 149 Turkey     |
| 121 TMATEPDPI V 130  | 131 QVDRKPKCCF 140   | 141 FS FSPKIQAN 150 Zebrafish |
| 151 KVVKAQLW IY 160  | 161 LRP VKTPTTV 170  | 171 FVQILRLIKP 180 Mouse      |
| 151 KVVKAQLW IY 160  | 161 LRAVKTPTTV 170   | 171 FVQILRLIKP 180 Rat        |
| 150 KVVKAQLW IY 159  | 160 LRP VETPTTV 169  | 170 FVQILRLIKP 179 Human      |
| 150 KVVKAQLW IY 159  | 160 LRP VETPTTV 169  | 170 FVQILRLIKP 179 Baboon     |
| 150 KLVKAQLW IY 159  | 160 LRP VKTPATV 169  | 170 FVQILRLIKP 179 Bovine     |
| 150 KVVKAQLW IY 159  | 160 LRP VKTPTTV 169  | 170 FVQILRLIKP 179 Porcine    |
| 150 KVVKAQLW IY 159  | 160 LRP VKTPTTV 169  | 170 FVQILRLIKP 179 Ovine      |
| 150 KVVKAQLW IY 159  | 160 LRQVQKPTTV 169   | 170 FVQILRLIKP 179 Chicken    |
| 150 KVVKAQLW IY 159  | 160 LRQVQKPTTV 169   | 170 FVQILRLIKP 179 Turkey     |
| 151 R I VRAQLWVH 160 | 161 LRP AEEATTV 169  | 170 FLQISRLM-P 179 Zebrafish  |
| 181 MKDGTRYTGI 190   | 191 RSLKLDMSPG 200   | 201 TGIWQSIDVK 210 Mouse      |
| 181 MKDGTRYTGI 190   | 191 RSLKLDMSPG 200   | 201 TGIWQSIDVK 210 Rat        |
| 180 MKDGTRYTGI 189   | 190 RSLKLDMNPG 199   | 200 TGIWQSIDVK 209 Human      |
| 180 MKDGTRYTGI 189   | 190 RSLKLDMNPG 199   | 200 TGIWQSIDVK 209 Baboon     |
| 180 MKDGTRYTGI 189   | 190 RSLKLDMNPG 199   | 200 TGIWQSIDVK 209 Bovine     |
| 180 MKDGTRYTGI 189   | 190 RSLKLDMNPG 199   | 200 TGIWQSIDVK 209 Porcine    |
| 180 MKDGTRYTGI 189   | 190 RSLKLDMNPG 199   | 200 TGIWQSIDVK 209 Ovine      |
| 180 MKDGTRYTGI 189   | 190 RSLKLDMNPG 199   | 200 TGIWQSIDVK 209 Chicken    |
| 180 MKDGTRYTGI 189   | 190 RSLKLDMNPG 199   | 200 TGIWQSIDVK 209 Turkey     |
| 180 V KDGGRRH-I 188  | 189 RSLK IDV NAG 198 | 199 VTSWQSIDVK 208 Zebrafish  |
| 211 TVLQNWLKQP 220   | 221 ESNLGIEIKA 230   | 231 LD ENGHDLAV 240 Mouse     |
| 211 TVLQNWLKQP 220   | 221 ESNLGIEIKA 230   | 231 LD ENGHDLAV 240 Rat       |
| 210 TVLQNWLKQP 219   | 220 ESNLGIEIKA 229   | 230 LD ENGHDLAV 239 Human     |
| 210 TVLQNWLKQP 219   | 220 ESNLGIEIKA 229   | 230 LD ENGHDLAV 239 Baboon    |
| 210 TVLQNWLKQP 219   | 220 ESNLGIEIKA 229   | 230 LD ENGHDLAV 239 Bovine    |
| 210 TVLQNWLKQP 219   | 220 ESNLGIEIKA 229   | 230 LD ENGHDLAV 239 Porcine   |
| 210 TVLQNWLKQP 219   | 220 ESNLGIEIKA 229   | 230 LD ENGHDLAV 239 Ovine     |
| 210 TVLQNWLKQP 219   | 220 ESNLGIEIKA 229   | 230 FD ETGRDLAV 239 Chicken   |
| 210 TVLQNWLKQP 219   | 220 ESNLGIEIKA 229   | 230 FD ENGRDLAV 239 Turkey    |
| 209 QVLTVWLKQP 218   | 219 ETNRGIEINA 228   | 229 YDAKGNDLAV 238 Zebrafish  |

FIG. 1B



|                      |                      |                               |
|----------------------|----------------------|-------------------------------|
| 241 TFPGPGE DGL 250  | 251 NPFLEV K VTD 260 | 261 TPKRSRRDFG 270 Mouse      |
| 241 TFPGPGE DGL 250  | 251 NPFLEV K VTD 260 | 261 TPKRSRRDFG 270 Rat        |
| 240 TFPGPGE DGL 249  | 250 NPFLEV K VTD 259 | 260 TPKRSRRDFG 269 Human      |
| 240 TFPGPGE DGL 249  | 250 NPFLEV K VTD 259 | 260 TPKRSRRDFG 269 Baboon     |
| 240 TFPEPGE DGL 249  | 250 TPFLEV K VTD 259 | 260 TPKRSRRDFG 269 Bovine     |
| 240 TFPGPGE DGL 249  | 250 NPFLEV K VTD 259 | 260 TPKRSRRDFG 269 Porcine    |
| 240 TFPEPGE E GL 249 | 250 NPFLEV K VTD 259 | 260 TPKRSRRDFG 269 Ovine      |
| 240 TFPGPGE DGL 249  | 250 NPFLEV R VTD 259 | 260 TPKRSRRDFG 269 Chicken    |
| 240 TFPGPGE DGL 249  | 250 NPFLEV R VTD 259 | 260 TPKRSRRDFG 269 Turkey     |
| 239 TSTETGE DGL 248  | 249 LPFMEV KI SE 258 | 259 GPKRIR RDSG 268 Zebrafish |
| 271 LDCDEHSTES 280   | 281 RCCRYPLTV D 290  | 291 FEA FGWDWII 300 Mouse     |
| 271 LDCDEHSTES 280   | 281 RCCRYPLTV D 290  | 291 FEA FGWDWII 300 Rat       |
| 270 LDCDEHSTES 279   | 280 RCCRYPLTV D 289  | 290 FEA FGWDWII 299 Human     |
| 270 LDCDEHSTES 279   | 280 RCCRYPLTV D 289  | 290 FEA LGWDWII 299 Baboon    |
| 270 LDCDEHSTES 279   | 280 RCCRYPLTV D 289  | 290 FEA FGWDWII 299 Bovine    |
| 270 LDCDEHSTES 279   | 280 RCCRYPLTV D 289  | 290 FEA FGWDWII 299 Porcine   |
| 270 LDCDEHSTES 279   | 280 RCCRYPLTV D 289  | 290 FEA FGWDWII 299 Ovine     |
| 270 LDCDEHSTES 279   | 280 RCCRYPLTV D 289  | 290 FEA FGWDWII 299 Chicken   |
| 270 LDCDEHSTES 279   | 280 RCCRYPLTV D 289  | 290 FEA FGWDWII 299 Turkey    |
| 269 LDCDEN SSES 278  | 279 RCCRYPLTV D 288  | 289 FEDFGWDWII 298 Zebrafish  |
| 301 APKRYKANYC 310   | 311 SGECE FV FLQ 320 | 321 KYPTH L VHQ 330 Mouse     |
| 301 APKRYKANYC 310   | 311 SGECE FV FLQ 320 | 321 KYPTH L VHQ 330 Rat       |
| 300 APKRYKANYC 309   | 310 SGECE FV FLQ 319 | 320 KYPTH L VHQ 329 Human     |
| 300 APKRYKANYC 309   | 310 SGECE FV FLQ 319 | 320 KYPTH L VHQ 329 Baboon    |
| 300 APKRYKANYC 309   | 310 SGECE FV FLQ 319 | 320 KYPTH L VHQ 329 Bovine    |
| 300 APKRYKANYC 309   | 310 SGECE FV FLQ 319 | 320 KYPTH L VHQ 329 Porcine   |
| 300 APKRYKANYC 309   | 310 SGECE FL FLQ 319 | 320 KYPTH L VHQ 329 Ovine     |
| 300 APKRYKANYC 309   | 310 SGECE FV FLQ 319 | 320 KYPTH L VHQ 329 Chicken   |
| 300 APKRYKANYC 309   | 310 SGECE FV FLQ 319 | 320 KYPTH L VHQ 329 Turkey    |
| 299 APKRYKANYC 308   | 309 SGECDYMYLQ 318   | 319 KYPTH L VNK 328 Zebrafish |
| 331 ANPRGSAGPC 340   | 341 CTPTKMSPIN 350   | 351 MLYFNGKEQI 360 Mouse      |
| 331 ANPRGSAGPC 340   | 341 CTPTKMSPIN 350   | 351 MLYFNGKEQI 360 Rat        |
| 330 ANPRGSAGPC 339   | 340 CTPTKMSPIN 349   | 350 MLYFNGKEQI 359 Human      |
| 330 ANPRGSAGPC 339   | 340 CTPTKMSPIN 349   | 350 MLYFNGKEQI 359 Baboon     |
| 330 ANPRGSAGPC 339   | 340 CTPTKMSPIN 349   | 350 MLYFNGEGQI 359 Bovine     |
| 330 ANPRGSAGPC 339   | 340 CTPTKMSPIN 349   | 350 MLYFNGKEQI 359 Porcine    |
| 330 ANPKGSAGPC 339   | 340 CTPTKMSPIN 349   | 350 MLYFNGKEQI 359 Ovine      |
| 330 ANPRGSAGPC 339   | 340 CTPTKMSPIN 349   | 350 MLYFNGKEQI 359 Chicken    |
| 330 ANPRGSAGPC 339   | 340 CTPTKMSPIN 349   | 350 MLYFNGKEQI 359 Turkey     |
| 329 ASPRGTAGPC 338   | 339 CTPTKMSPIN 248   | 349 MLYFNGKEQI 359 Zebrafish  |

FIG. 1C



|                     |                          |
|---------------------|--------------------------|
| 361 IYGKIPAMVV 370  | 371 DRCGCS 376 Mouse     |
| 361 IYGKIPAMVV 370  | 371 DRCGCS 376 Rat       |
| 360 IYGKIPAMVV 369  | 370 DRCGCS 375 Human     |
| 360 IYGKIPAMVV 369  | 370 DRCGCS 375 Baboon    |
| 360 IYGKIPAMVV 369  | 370 DRCGCS 375 Bovine    |
| 360 IYGKIPAMVV 369  | 370 DRCGCS 375 Porcine   |
| 360 IYGKIPAMVV 369  | 370 DRCGCS 375 Ovine     |
| 360 IYGKIPAMVV 369  | 370 DRCGCS 375 Chicken   |
| 360 IYGKIPAMVV 369  | 370 DRCGCS 375 Turkey    |
| 359 IYGKIP SMVV 368 | 369 DRCGCS 374 Zebrafish |

**FIG. 1D**

FIG. 2

FIG. 3

FIG. 4



10 20 30 40  
 GGA TCC AAA CGT TAT AAA GCT AAC TAT TGC TCT GGT GAA TGC GAA  
 Gly Ser Lys Arg Tyr Lys Ala Asn Tyr Cys Ser Gly Glu Cys Glu  
 50  
 TTC AGA TCT  
 Phe Arg Ser

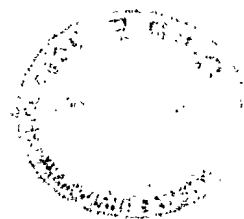
FIG. 5

10 20 30 40  
 GGA TCC GAA TTC GTT TTC CTG CAG AAA TAT CCG CAT ACC CAT CTG  
 Gly Ser Glu Phe Val Phe Leu Gln Lys Tyr Pro His Thr His Leu  
 50 60 70  
 GTT CAT CAG GCT AAC CCG CGT AGA TCT  
 Val His Gln Ala Asn Pro Arg Arg Ser

FIG. 6

10 20 30 40  
 GGA TCC GCT GGT CCG TGC TGT TAT CCG ACC AAA ATG TCT CCG ATC  
 Gly Ser Ala Gly Pro Cys Cys Tyr Pro Thr Lys MET Ser Pro Ile  
 50 60 70 80  
 AAC ATG CTG TAT TTC AAC GGT GAA TGC CAG AGA TCT  
 Asn MET Leu Tyr Phe Asn Gly Glu Cys Gln Arg Ser

FIG. 7



10 20 30 40  
 GGA TCC GAA TGC CAG ATC ATT TAT TGC AAA ATC CCG GCT ATG GTT  
 Gly Ser Glu Cys Gln Ile Ile Tyr Cys Lys Ile Pro Ala MET Val

50 60 70  
 GTA GAC CGT TGC GGT TGT TCT AGA TCT  
 Val Asp Arg Cys Gly Cys Ser Arg Ser

FIG. 8

10 20 30 40  
 GGA TCC GAA CAG AAA GAA AAC GTT GAA AAA GAA GGT CTG TGC AAC  
 Gly Ser Glu Gln Lys Glu Asn Val Glu Lys Glu Gly Leu Cys Asn

50 60  
 GCT TGC CTG TGG AGA TCT  
 Ala Cys Leu Trp Arg Ser

FIG. 9

10 20 30 40  
 GGA TCC CAT GAC CTG GCT GTT ACC TTC CCG GAA CCG GGT GAA GAC  
 Gly Ser His Asp Leu Ala Val Thr Phe Pro Glu Pro Gly Glu Asp

50 60  
 GGT CTG ACC AGA TCT  
 Gly Leu Thr Arg Ser

FIG. 10



|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |    |  |    |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|--|----|--|
|     |     |     | 10  |     |     |     | 20  |     |     |     | 30  |     |     |     | 40 |  |    |  |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |    |  |    |  |
| GGA | TCC | ACC | CCG | TTC | CTG | GAA | GTT | AAA | GTT | ACC | GAC | ACT | CCG | AAA |    |  |    |  |
| Gly | Ser | Thr | Pro | Phe | Leu | Glu | Val | Lys | Val | Thr | Asp | Thr | Pro | Lys |    |  |    |  |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |    |  |    |  |
|     |     |     | 50  |     |     |     |     |     |     |     |     |     |     |     |    |  | 60 |  |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |    |  |    |  |
| CGT | TCT | CGT | AGA | TCT |     |     |     |     |     |     |     |     |     |     |    |  |    |  |
| Arg | Ser | Arg | Arg | Ser |     |     |     |     |     |     |     |     |     |     |    |  |    |  |

FIG. 11

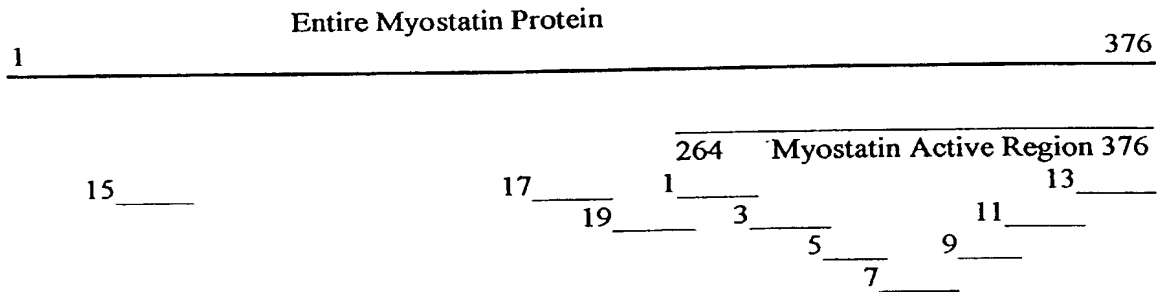


FIG. 12



10 20 30 40  
 GGA TCC CGT TCT CGT CGC GAC TTT GGT CTG GAC TGC GAC GAA CAT  
 Gly Ser Arg Ser Arg Arg Asp Phe Gly Leu Asp Cys Asp Glu His

50 60 70 80 90  
 TCT ACC GAA AGA TCC TCT CGT TGC TGT CGC TAT CCG CTG ACC GTT  
 Ser Thr Glu Arg Ser Ser Arg Cys Cys Arg Tyr Pro Leu Thr Val

100 110 120 130  
 GAC TTC GAA GCT TTT GGT TGG GAC TGG ATC ATT GCA CCG AAA CGT  
 Asp Phe Glu Ala Phe Gly Trp Asp Trp Ile Ile Ala Pro Lys Arg

140 150 160 170 180  
 TAT AGA TCC AAA CGT TAT AAA GCT AAC TAT TGC TCT GGT GAA TGC  
 Tyr Arg Ser Lys Arg Tyr Lys Ala Asn Tyr Cys Ser Gly Glu Cys

190 200 210 220  
 GAA TTC GTT TTC CTG CAG AAA TAT CCG CAT ACC CAT CTG GTT CAT  
 Glu Phe Val Phe Leu Gln Lys Tyr Pro His Thr His Leu Val His

230 240 250 260 270  
 CAG GCT AAC CCG CGT AGA TCC GCT GGT CCG TGC TGT TAT CCG ACC  
 Gln Ala Asn Pro Arg Arg Ser Ala Gly Pro Cys Cys Tyr Pro Thr

280 290 300 310  
 AAA ATG TCT CCG ATC AAC ATG CTG TAT TTC AAC GGT GAA TGC CAG  
 Lys MET Ser Pro Ile Asn MET Leu Tyr Phe Asn Gly Glu Cys Gln

320 330 340 350 360  
 ATC ATT TAT TGC AAA ATC CCG GCT ATG GTT GTA GAC CGT TGC GGT  
 Ile Ile Tyr Cys Lys Ile Pro Ala MET Val Val Asp Arg Cys Gly

370  
 TGT TCT AGA TCT  
 Cys Ser Arg Ser

FIG. 13

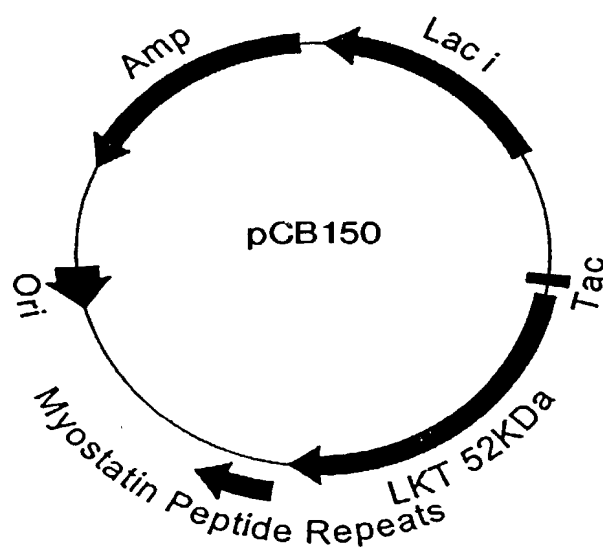


FIG. 14

1870                    1880                    1890                    1900                    1910  
 : ATG GCT ACT GTT ATA GAT CTA AGC TTC CCA AAA ACT GGG GCA AAA  
 : MET Ala Thr Val Ile Asp Leu Ser Phe Pro Lys Thr Gly Ala Lys

1920                    1930                    1940                    1950  
 : AAA ATT ATC CTC TAT ATT CCC CAA AAT TAC CAA TAT GAT ACT GAA  
 : Lys Ile Ile Leu Tyr Ile Pro Gln Asn Tyr Gln Tyr Asp Thr Glu

1960                    1970                    1980                    1990                    2000  
 : CAA GGT AAT GGT TTA CAG GAT TTA GTC AAA GCG GCC GAA GAG TTG  
 : Gln Gly Asn Gly Leu Gln Asp Leu Val Lys Ala Ala Glu Glu Leu

2010                    2020                    2030                    2040  
 : GGG ATT GAG GTA CAA AGA GAA GAA CGC AAT AAT ATT GCA ACA GCT  
 : Gly Ile Glu Val Gln Arg Glu Glu Arg Asn Asn Ile Ala Thr Ala

2050                    2060                    2070                    2080                    2090  
 : CAA ACC AGT TTA GGC ACG ATT CAA ACC GCT ATT GGC TTA ACT GAG  
 : Gln Thr Ser Leu Gly Thr Ile Gln Thr Ala Ile Gly Leu Thr Glu

2100                    2110                    2120                    2130  
 : CGT GGC ATT GTG TTA TCC GCT CCA CAA ATT GAT AAA TTG CTA CAG  
 : Arg Gly Ile Val Leu Ser Ala Pro Gln Ile Asp Lys Leu Leu Gln

2140                    2150                    2160                    2170                    2180  
 : AAA ACT AAA GCA GGC CAA GCA TTA GGT TCT GCC GAA AGC ATT GTA  
 : Lys Thr Lys Ala Gly Gln Ala Leu Gly Ser Ala Glu Ser Ile Val

2190                    2200                    2210                    2220  
 : CAA AAT GCA AAT AAA GCC AAA ACT GTA TTA TCT GGC ATT CAA TCT  
 : Gln Asn Ala Asn Lys Ala Lys Thr Val Leu Ser Gly Ile Gln Ser

2230                    2240                    2250                    2260                    2270  
 : ATT TTA GGC TCA GTA TTG GCT GGA ATG GAT TTA GAT GAG GCC TTA  
 : Ile Leu Gly Ser Val Leu Ala Gly MET Asp Leu Asp Glu Ala Leu

FIG. 15A

2280                      2290                      2300                      2310  
 CAG AAT AAC AGC AAC CAA CAT GCT CTT GCT AAA GCT GGC TTG GAG  
 Gln Asn Asn Ser Asn Gln His Ala Leu Ala Lys Ala Gly Leu Glu

2320                      2330                      2340                      2350                      2360  
 CTA ACA AAT TCA TTA ATT GAA AAT ATT GCT AAT TCA GTA AAA ACA  
 Leu Thr Asn Ser Leu Ile Glu Asn Ile Ala Asn Ser Val Lys Thr

2370                      2380                      2390                      2400  
 CTT GAC GAA TTT GGT GAG CAA ATT AGT CAA TTT GGT TCA AAA CTA  
 Leu Asp Glu Phe Gly Glu Gln Ile Ser Gln Phe Gly Ser Lys Leu

2410                      2420                      2430                      2440                      2450  
 CAA AAT ATC AAA GGC TTA GGG ACT TTA GGA GAC AAA CTC AAA AAT  
 Gln Asn Ile Lys Gly Leu Gly Thr Leu Gly Asp Lys Leu Lys Asn

2460                      2470                      2480                      2490  
 ATC GGT GGA CTT GAT AAA GCT GGC CTT GGT TTA GAT GTT ATC TCA  
 Ile Gly Gly Leu Asp Lys Ala Gly Leu Gly Leu Asp Val Ile Ser

2500                      2510                      2520                      2530                      2540  
 GGG CTA TTA TCG GGC GCA ACC GCT GCA CTT GTA CTT GCA GAT AAA  
 Gly Leu Leu Ser Gly Ala Thr Ala Ala Leu Val Leu Ala Asp Lys

2550                      2560                      2570                      2580  
 AAT GCT TCA ACA GCT AAA AAA GTG GGT GCG GGT TTT GAA TTG GCA  
 Asn Ala Ser Thr Ala Lys Lys Val Gly Ala Gly Phe Glu Leu Ala

2590                      2600                      2610                      2620                      2630  
 AAC CAA GTT GTT GGT AAT ATT ACC AAA GCC GTT TCT TCT TAC ATT  
 Asn Gln Val Val Gly Asn Ile Thr Lys Ala Val Ser Ser Tyr Ile

2640                      2650                      2660                      2670  
 TTA GCC CAA CGT GTT GCA GCA GGT TTA TCT TCA ACT GGG CCT GTG  
 Leu Ala Gln Arg Val Ala Ala Gly Leu Ser Ser Thr Gly Pro Val

FIG. 15B

2680            2690            2700            2710            2720  
 GCT GCT TTA ATT GCT TCT ACT GTT TCT CTT GCG ATT AGC CCA TTA  
 Ala Ala Leu Ile Ala Ser Thr Val Ser Leu Ala Ile Ser Pro Leu  
  
 2730            2740            2750            2760  
 GCA TTT GCC GGT ATT GCC GAT AAA TTT AAT CAT GCA AAA AGT TTA  
 Ala Phe Ala Gly Ile Ala Asp Lys Phe Asn His Ala Lys Ser Leu  
  
 2770            2780            2790            2800            2810  
 GAG AGT TAT GCC GAA CGC TTT AAA AAA TTA GGC TAT GAC GGA GAT  
 Glu Ser Tyr Ala Glu Arg Phe Lys Lys Leu Gly Tyr Asp Gly Asp  
  
 2820            2830            2840            2850  
 AAT TTA TTA GCA GAA TAT CAG CGG GGA ACA GGG ACT ATT GAT GCA  
 Asn Leu Leu Ala Glu Tyr Gln Arg Gly Thr Gly Thr Ile Asp Ala  
  
 2860            2870            2880            2890            2900  
 TCG GTT ACT GCA ATT AAT ACC GCA TTG GCC GCT ATT GCT GGT GGT  
 Ser Val Thr Ala Ile Asn Thr Ala Leu Ala Ala Ile Ala Gly Gly  
  
 2910            2920            2930            2940  
 GTG TCT GCT GCT GCA GCC GAT TTA ACA TTT GAA AAA GTT AAA CAT  
 Val Ser Ala Ala Ala Ala Asp Leu Thr Phe Glu Lys Val Lys His  
  
 2950            2960            2970            2980            2990  
 AAT CTT GTC ATC ACG AAT AGC AAA AAA GAG AAA GTG ACC ATT CAA  
 Asn Leu Val Ile Thr Asn Ser Lys Lys Glu Lys Val Thr Ile Gln  
  
 3000            3010            3020            3030  
 AAC TGG TTC CGA GAG GCT GAT TTT GCT AAA GAA GTG CCT AAT TAT  
 Asn Trp Phe Arg Glu Ala Asp Phe Ala Lys Glu Val Pro Asn Tyr  
  
 3040            3050            3060            3070            3080  
 AAA GCA ACT AAA GAT GAG AAA ATC GAA GAA ATC ATC GGT CAA AAT  
 Lys Ala Thr Lys Asp Glu Lys Ile Glu Glu Ile Ile Gly Gln Asn

FIG. 15C

3090                    3100                    3110                    3120  
 GGC GAG CGG ATC ACC TCA AAG CAA GTT GAT GAT CTT ATC GCA AAA  
 Gly Glu Arg Ile Thr Ser Lys Gln Val Asp Asp Leu Ile Ala Lys  
  
 3130                    3140                    3150                    3160                    3170  
 GGT AAC GGC AAA ATT ACC CAA GAT GAG CTA TCA AAA GTT GTT GAT  
 Gly Asn Gly Lys Ile Thr Gln Asp Glu Leu Ser Lys Val Val Asp  
  
 3180                    3190                    3200                    3210  
 AAC TAT GAA TTG CTC AAA CAT AGC AAA AAT GTG ACA AAC AGC TTA  
 Asn Tyr Glu Leu Leu Lys His Ser Lys Asn Val Thr Asn Ser Leu  
  
 3220                    3230                    3240                    3250                    3260  
 GAT AAG TTA ATC TCA TCT GTA AGT GCA TTT ACC TCG TCT AAT GAT  
 Asp Lys Leu Ile Ser Ser Val Ser Ala Phe Thr Ser Ser Asn Asp  
  
 3270                    3280                    3290                    3300  
 TCG AGA AAT GTA TTA GTG GCT CCA ACT TCA ATG TTG GAT CAA AGT  
 Ser Arg Asn Val Leu Val Ala Pro Thr Ser MET Leu Asp Gln Ser  
  
 3310                    3320                    3330                    3340  
 TTA TCT TCT CTT CAA TTT GCT AGG GGA TCC TAG  
 Leu Ser Ser Leu Gln Phe Ala Arg Gly Ser ---

FIG. 15D

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1  ATGCAAAAAC  TGCAAATCTC  TGTTTATATT  TACCTATTTA  CGCTGATTGT
51  TGCTGGCCCA  GTGGATCTGA  ATGAGAACAG  CGAGCAGAAG  GAAAATGTGG
101  AAAAAGAGGG  GCTGTGTAAT  GCATGTTTGT  GGAGGGAAAA  CACTACATCC
151  TCAAGACTAG  AAGCCATAAA  AATCCAAATC  CTCAGTAAAC  TTCGCCCTGGA
201  AACAGCTCCT  AACATCAGCA  AAGATGCTAT  CAGACAACTT  TTGCCCAAGG
251  CTCCTCCACT  CCTGGAACCTG  ATTGATCAGT  TCGATGTCCA  GAGAGATGCC
301  AGCAGTGACG  GCTCCTTGGA  AGACGATGAC  TACCACGCCA  GGACGGAAAC
351  GGTCAATTACC  ATGCCCACGG  AGTCTGATCT  TCTAACGCAA  GTGGAAGGAA
401  AACCCAAATG  TTGCTTC'TTT  AAATTTAGCT  CTAAGATACA  ATACAATAAA
451  CTAGTAAAGG  CCCAACTGTG  GATATATCTG  AGGCCTGTCA  AGACTCCTGC
501  GACAGTGTTT  GTGCAAATCC  TGAGACTCAT  CAAACCCATG  AAAGACGGTA
551  CAAGGTATAC  TGGAATCCGA  TCTCTGAAAC  TTGACATGAA  CCCAGGCACT
601  GGTATTTGGC  AGAGCATTTGA  TGTGAAGACA  GTGTTGCAGA  ACTGGCTCAA
651  ACAACCTGAA  TCCAACTTAG  GCATTGAAAT  CAAAGCTTTA  GATGAGAATG
701  GCCATGATCT  TGCTGTAACC  TTCCCAGAAC  CAGGAGAAGA  TGGACTGACT
751  CCTTTTTTAG  AAGTCAAGGT  AACAGACACA  CAAAAAAGAT  CTAGGAGAGA
801  TTTTGGGCTT  GATTGTGATG  AACACTCCAC  AGAATCTCGA  TGCTGTGCGT
851  ACCCCCTCAC  GGTGGATTTT  GAAGCTTTTG  GATGGGATTG  GATTATTGCA
901  CCTAAAAGAT  ATAAGGCCAA  T'ACTGCTCT  GGAGAATGTG  AATTTGTATT
951  TTTGCAAAAG  TATCCTCATA  CCCATCTTGT  GCACCAAGCA  AACCCCAGAG
1001  GTTCAGCCGG  CCCCTGCTGT  ACTCCTACAA  AGATGTCTCC  AATTAATATG
1051  CTATATTTTA  ATGGCGAAGG  ACAAATAATA  TACGGGAAGA  TTCCAGCCAT
1101  GGTAGTAGAT  CGCTGTGGGT  GCTCATGA

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FIG. 16A

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1  MQKLQISVYI  YLFTLIVAGP  VDLNENSEQK  ENVEKEGLCN  ACLWRENTTS
51  SRLEAIKIQI  LSKLRLETAP  NISKDAIRQL  LPKAPLLEL  IDQFDVQRDA
101  SSDGSLEDDD  YHARTETVIT  MPTESDLLTQ  VEGKPKCCFF  KFSSKIQYNK
151  LVKAQLWIYL  RPVKTPATVF  VQILRLIKPM  KDGTRYTGIR  SLKLDMPNGT
201  GIWQSIDVKT  VLQNLWKQPE  SNLGIEIKAL  DENGHD LAVT  FPEPGEDGLT
251  PFLEVKVTDI  PKRSRRDFGL  DCDEHSTESR  CCRYPLTVDF  EAFGWDWIIA
301  PKRYKANYCS  GECEVFLQK  YPHTHLVHQA  NPRGSAGPCC  TPTKMSPINM
351  LYFNNEGQII  YGKIPAMVVD  RCGCS

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FIG. 16B

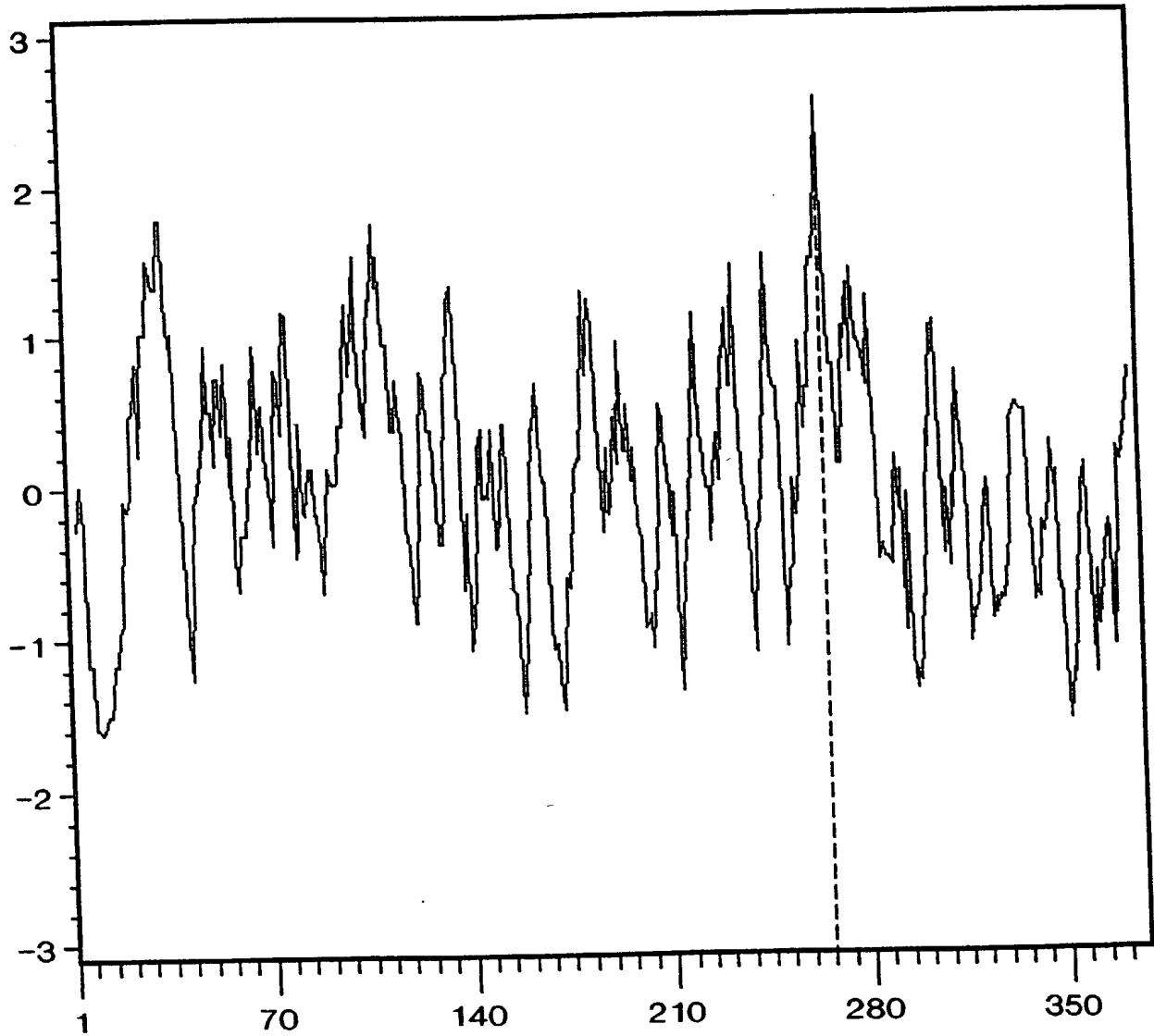


FIG. 17



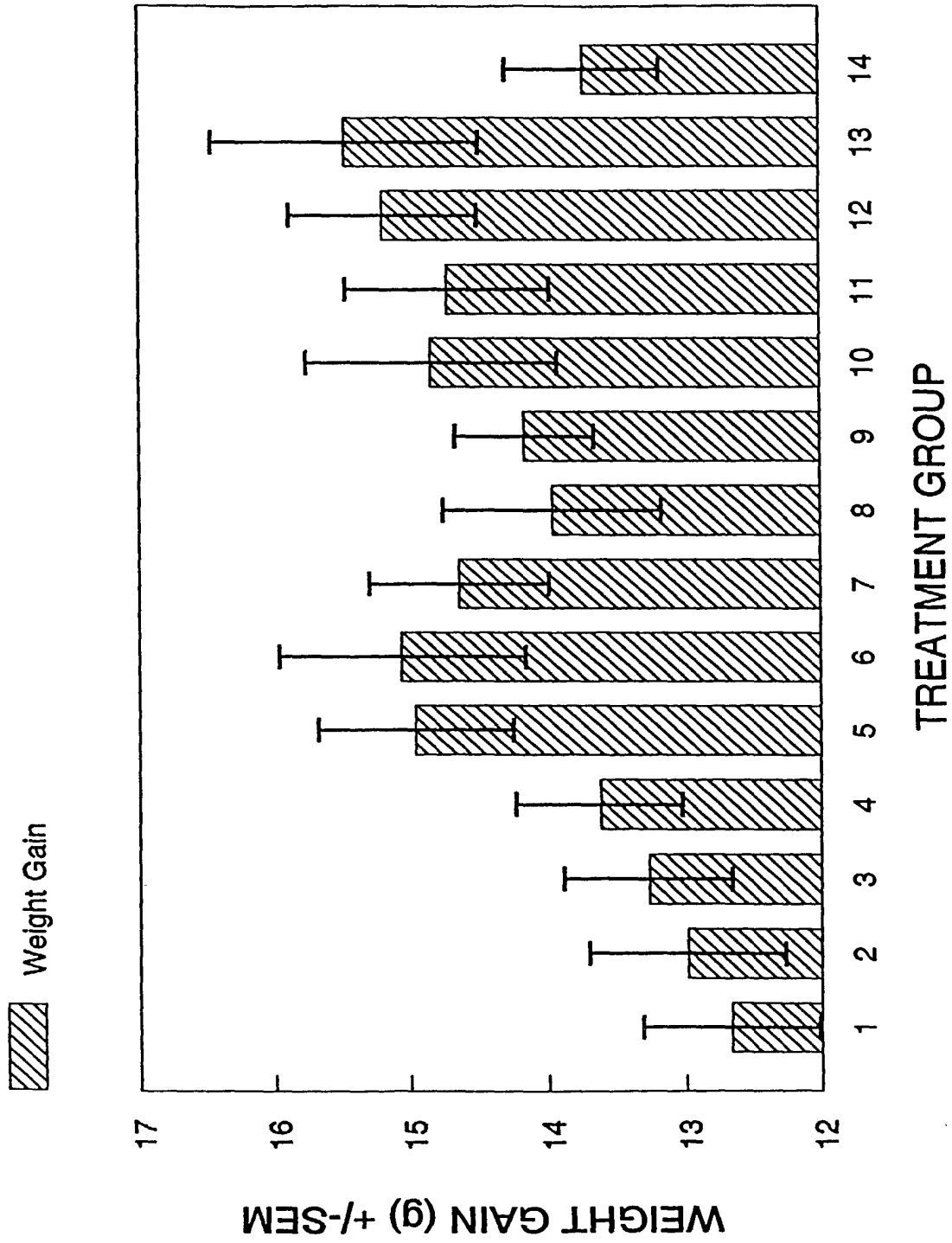


FIG. 18